

0590
7905

O/PE

CRF Errors Corrected by the STIC Systems Branch

CRF Processing Date: 10/17/2001
Edited by: A
Verified by: (STIC stat

Serial Number: 09/934,249

ENTERED

#2

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEO ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEO ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seq 16 inserted hard return

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 3/1/95

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/934,249

DATE: 10/17/2001

TIME: 12:05:07

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10172001\I934249.raw

4 <110> APPLICANT: Lee, Richard T.
5 Landschulz, Katherine T.
6 Turi, Thomas G.
7 Thompson, John F.
8 Kennedy, Scott P.

10 <120> TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
11 CARDIOVASCULAR CONDITIONS

13 <130> FILE REFERENCE: P0738/7001/ERP/KA

C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/934,249

C--> 15 <141> CURRENT FILING DATE: 2001-08-21

15 <150> PRIOR APPLICATION NUMBER: US 60/227,159

16 <151> PRIOR FILING DATE: 2000-08-22

18 <160> NUMBER OF SEQ ID NOS: 17

20 <170> SOFTWARE: FastSEQ for Windows Version 3.0

22 <210> SEQ ID NO: 1

23 <211> LENGTH: 1321

24 <212> TYPE: DNA

25 <213> ORGANISM: Homo Sapiens

27 <220> FEATURE:

28 <221> NAME/KEY: CDS

29 <222> LOCATION: (413)...(1273)

31 <400> SEQUENCE: 1

32	cgaccgcggt ctcggagcga aacccgatct ccttggactt gaatgaggag gaggaggcgg	60
33	cggcggcggc ggcggcggag gcgctcggct ggggaaagct agcggcagag gctcagcccc	120
34	ggcggcagcg cgcgccccgc tgccagccca ttttccggac gccaccccgcg ggcaactgccg	180
35	acgcccccgcg ggctgccgag gggaggccgg gggggcgcgag cggagcgcgg tcccgcgcac	240
36	tgagccccgc ggcgcccccg gaacttggcg gcgacccgag cccggcgagc cggggcgcg	300
37	ctcccccgcc gcgcgcctcc tgcattgcgg gccccagctc cgggcgcgg ccggagcccc	360
38	ccccggcgcc ccccgagccc cccgcgcccc gcgcgcgcgc gccgcgcggt cc atg cac	418
39		Met His
40		1
42	cgc ttg atg ggg gtc aac agc acc gcc gcc gcc gcc gcc ggg cag ccc	466
43	Arg Leu Met Gly Val Asn Ser Thr Ala Ala Ala Ala Ala Gly Gln Pro	
44	5 10 15	
46	aat gtc tcc tgc acg tgc aac tgc aaa cgc tct ttg ttc cag agc atg	514
47	Asn Val Ser Cys Thr Cys Asn Cys Lys Arg Ser Leu Phe Gln Ser Met	
48	20 25 30	
50	gag atc acg gag ctg gag ttt gtt cag atc atc atc atc gtg gtg gtg	562
51	Glu Ile Thr Glu Leu Glu Phe Val Gln Ile Ile Ile Ile Val Val Val	
52	35 40 45 50	
54	atg atg gtg atg gtg gtg gtg atc acg tgc ctg ctg agc cac tac aag	610
55	Met Met Val Met Val Val Val Ile Thr Cys Leu Leu Ser His Tyr Lys	
56	55 60 65	
58	ctg tct gca cgg tcc ttc atc agc cgg cac agc cag ggg cgg agg aga	658
59	Leu Ser Ala Arg Ser Phe Ile Ser Arg His Ser Gln Gly Arg Arg Arg	
60	70 75 80	
62	gaa gat gcc ctg tcc tca gaa gga tgc ctg tgg ccc tcg gag agc aca	706

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10172001\I934249.raw

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63  Glu Asp Ala Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser Glu Ser Thr
64      85          90          95
66  gtg tca ggc aac gga atc cca gag ccg cag gtc tac gcc ccg cct cgg      754
67  Val Ser Gly Asn Gly Ile Pro Glu Pro Gln Val Tyr Ala Pro Pro Arg
68      100          105          110
70  ccc acc gac cgc ctg gcc gtg ccg ccc ttc gcc cag cgg gag cgc ttc      802
71  Pro Thr Asp Arg Leu Ala Val Pro Pro Phe Ala Gln Arg Glu Arg Phe
72  115          120          125          130
74  cac cgc ttc cag ccc acc tat ccg tac ctg cag cac gag atc gac ctg      850
75  His Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile Asp Leu
76      135          140          145
78  cca ccc acc atc tcg ctg tca gac ggg gag gag ccc cca ccc tac cag      898
79  Pro Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro Tyr Gln
80      150          155          160
82  ggc ccc tgc acc ctc cag ctt cgg gac ccc gag cag cag ctg gaa ctg      946
83  Gly Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu Glu Leu
84      165          170          175
86  aac cgg gag tcg gtg cgc gca ccc cca aac aga acc atc ttc gac agt      994
87  Asn Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe Asp Ser
88      180          185          190
90  gac ctg atg gat agt gcc agg ctg ggc ggc ccc tgc ccc ccc agc agt      1042
91  Asp Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro Ser Ser
92  195          200          205          210
94  aac tcg ggc atc agc gcc acg tgc tac ggc agc ggc ggg cgc atg gag      1090
95  Asn Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg Met Glu
96      215          220          225
98  ggg ccg ccg ccc acc tac agc gag gtc atc ggc cac tac ccg ggg tcc      1138
99  Gly Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro Gly Ser
100      230          235          240
102  tcc ttc cag cac cag cag agc agt ggg ccg ccc tcc ttg ctg gag ggg      1186
103  Ser Phe Gln His Gln Gln Ser Ser Gly Pro Pro Ser Leu Leu Glu Gly
104      245          250          255
106  acc cgg ctc cac cac aca cac atc gcg ccc cta gag agc gca gcc atc      1234
107  Thr Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala Ala Ile
108      260          265          270
110  tgg agc aaa gag aag gat aaa cag aaa gga cac cct ctc taggggtcccc      1283
111  Trp Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu
112  275          280          285
114  agggggggccg ggctggggct gcgtaggtga aaaggcag      1321
116 <210> SEQ ID NO: 2
117 <211> LENGTH: 287
118 <212> TYPE: PRT
119 <213> ORGANISM: Homo Sapiens
121 <400> SEQUENCE: 2
122  Met His Arg Leu Met Gly Val Asn Ser Thr Ala Ala Ala Ala Ala Gly
123      1          5          10          15
124  Gln Pro Asn Val Ser Cys Thr Cys Asn Cys Lys Arg Ser Leu Phe Gln
125      20          25          30
126  Ser Met Glu Ile Thr Glu Leu Glu Phe Val Gln Ile Ile Ile Ile Val

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```

127          35          40          45
128 Val Val Met Met Val Met Val Val Val Ile Thr Cys Leu Leu Ser His
129          50          55          60
130 Tyr Lys Leu Ser Ala Arg Ser Phe Ile Ser Arg His Ser Gln Gly Arg
131 65          70          75          80
132 Arg Arg Glu Asp Ala Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser Glu
133          85          90          95
134 Ser Thr Val Ser Gly Asn Gly Ile Pro Glu Pro Gln Val Tyr Ala Pro
135          100          105          110
136 Pro Arg Pro Thr Asp Arg Leu Ala Val Pro Pro Phe Ala Gln Arg Glu
137          115          120          125
138 Arg Phe His Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile
139          130          135          140
140 Asp Leu Pro Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro
141 145          150          155          160
142 Tyr Gln Gly Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu
143          165          170          175
144 Glu Leu Asn Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe
145          180          185          190
146 Asp Ser Asp Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro
147          195          200          205
148 Ser Ser Asn Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg
149          210          215          220
150 Met Glu Gly Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro
151 225          230          235          240
152 Gly Ser Ser Phe Gln His Gln Gln Ser Ser Gly Pro Pro Ser Leu Leu
153          245          250          255
154 Glu Gly Thr Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala
155          260          265          270
156 Ala Ile Trp Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu
157          275          280          285

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159 <210> SEQ ID NO: 3

160 <211> LENGTH: 861

161 <212> TYPE: DNA

162 <213> ORGANISM: Homo Sapiens

164 <220> FEATURE:

165 <221> NAME/KEY: CDS

166 <222> LOCATION: (1)...(861)

168 <400> SEQUENCE: 3

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169 atgcaccgct tgatgggggt caacagcacc gccgccgccg ccgccgggca gcccaatgtc      60
170 tcctgcacgt gcaactgcaa acgctctttg ttccagagca tggagatcac ggagctggag      120
171 tttgttcaga tcatcatcat cgtgggtggtg atgatggtga tgggtggtggt gatcacgtgc      180
172 ctgctgagcc actacaagct gtctgcacgg tccttcatca gccggcacag ccaggggagg      240
173 aggagagaag atgccctgtc ctcagaagga tgctgtggc cctcggagag cacagtgtca      300
174 ggcaacggaa tccagagacc gcaggtctac gcccgcctc ggcccaccga ccgctggcc      360
175 gtgcccgcct tcgcccagcg ggagcgcttc caccgcttc agcccaccta tccgtacctg      420
176 cagcacgaga tcgacctgcc acccaccatc tcgctgtcag acggggaggga gcccaccacc      480
177 taccagggcc cctgcaccct ccagcttcgg gaccccgagc agcagctgga actgaaccgg      540
178 gagtccggtgc gcgcaccccc aaacagaacc atcttcgaca gtgacctgat ggatagtgcc      600

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TIME: 12:05:07

Input Set : A:\PTO.AMC.txt

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```

179. aggctgggcg gcccctgccc cccagcagc aactcgggca tcagcgccac gtgctacggc 660
180. agcggcgggc gcatggaggg gccgcccgc acctacagcg aggtcatcgg ccactaccgc 720
181. gggctcctcct tccagcacca gcagagcagc gggccgccct ccttgctgga ggggacccgc 780
182. ctccaccaca cacacatcgc gcccctagag agcgcagcca tctggagcaa agagaaggat 840
183. aaacagaaag gacaccctct c 861
185 <210> SEQ ID NO: 4
186 <211> LENGTH: 477
187 <212> TYPE: DNA
188 <213> ORGANISM: Homo Sapiens
190 <220> FEATURE:
191 <221> NAME/KEY: CDS
192 <222> LOCATION: (7)...(474)
193 <223> OTHER INFORMATION: IEX1
195 <400> SEQUENCE: 4
196 ctcacc atg tgt cac tct cgc agc tgc cac ccg acc atg acc atc ctg 48
197 Met Cys His Ser Arg Ser Cys His Pro Thr Met Thr Ile Leu
198 1 5 10
200 cag gcc ccg acc ccg gcc ccc tcc acc atc ccg gga ccc cgg cgg ggc 96
201 Gln Ala Pro Thr Pro Ala Pro Ser Thr Ile Pro Gly Pro Arg Arg Gly
202 15 20 25 30
204 tcc ggt cct gag atc ttc acc ttc gac cct ctc ccg gag ccc gca gcg 144
205 Ser Gly Pro Glu Ile Phe Thr Phe Asp Pro Leu Pro Glu Pro Ala Ala
206 35 40 45
208 gcc cct gcc ggg cgc ccc agc gcc tct cgc ggg cac cga aag cgc agc 192
209 Ala Pro Ala Gly Arg Pro Ser Ala Ser Arg Gly His Arg Lys Arg Ser
210 50 55 60
212 cgc agg gtt ctc tac cct cga gtg gtc cgg cgc cag ctg cca gtc gag 240
213 Arg Arg Val Leu Tyr Pro Arg Val Val Arg Arg Gln Leu Pro Val Glu
214 65 70 75
216 gaa ccg aac cca gcc aaa agg ctt ctc ttt ctg ctg ctc acc atc gtc 288
217 Glu Pro Asn Pro Ala Lys Arg Leu Leu Phe Leu Leu Leu Thr Ile Val
218 80 85 90
220 ttc tgc cag atc ctg atg gct gaa gag ggt gtg ccg gcg ccc ctg cct 336
221 Phe Cys Gln Ile Leu Met Ala Glu Glu Gly Val Pro Ala Pro Leu Pro
222 95 100 105 110
224 cca gag gac gcc cct aac gcc gca tcc ctg gcg ccc acc cct gtg tcc 384
225 Pro Glu Asp Ala Pro Asn Ala Ala Ser Leu Ala Pro Thr Pro Val Ser
226 115 120 125
228 ccc gtc ctc gag ccc ttt aat ctg act tcg gag ccc tcg gac tac gct 432
229 Pro Val Leu Glu Pro Phe Asn Leu Thr Ser Glu Pro Ser Asp Tyr Ala
230 130 135 140
232 ctg gac ctc agc act ttc ctc cag caa cac ccg gcc gcc ttc 474
233 Leu Asp Leu Ser Thr Phe Leu Gln Gln His Pro Ala Ala Phe
234 145 150 155
236 taa 477
238 <210> SEQ ID NO: 5
239 <211> LENGTH: 156
240 <212> TYPE: PRT
241 <213> ORGANISM: Homo Sapiens

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RAW SEQUENCE LISTING

DATE: 10/17/2001

PATENT APPLICATION: US/09/934,249

TIME: 12:05:07

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10172001\I934249.raw

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243 <400> SEQUENCE: 5
244 Met Cys His Ser Arg Ser Cys His Pro Thr Met Thr Ile Leu Gln Ala
245 1 5 10 15
246 Pro Thr Pro Ala Pro Ser Thr Ile Pro Gly Pro Arg Arg Gly Ser Gly
247 20 25 30
248 Pro Glu Ile Phe Thr Phe Asp Pro Leu Pro Glu Pro Ala Ala Ala Pro
249 35 40 45
250 Ala Gly Arg Pro Ser Ala Ser Arg Gly His Arg Lys Arg Ser Arg Arg
251 50 55 60
252 Val Leu Tyr Pro Arg Val Val Arg Arg Gln Leu Pro Val Glu Glu Pro
253 65 70 75 80
254 Asn Pro Ala Lys Arg Leu Leu Phe Leu Leu Leu Thr Ile Val Phe Cys
255 85 90 95
256 Gln Ile Leu Met Ala Glu Glu Gly Val Pro Ala Pro Leu Pro Pro Glu
257 100 105 110
258 Asp Ala Pro Asn Ala Ala Ser Leu Ala Pro Thr Pro Val Ser Pro Val
259 115 120 125
260 Leu Glu Pro Phe Asn Leu Thr Ser Glu Pro Ser Asp Tyr Ala Leu Asp
261 130 135 140
262 Leu Ser Thr Phe Leu Gln Gln His Pro Ala Ala Phe
263 145 150 155
265 <210> SEQ ID NO: 6
266 <211> LENGTH: 2704
267 <212> TYPE: DNA
268 <213> ORGANISM: Homo Sapiens
270 <220> FEATURE:
271 <221> NAME/KEY: CDS
272 <222> LOCATION: (222)...(1394)
273 <223> OTHER INFORMATION: VDUPL
275 <400> SEQUENCE: 6
276 gcttagtgta accagcggcg tatatttttt aggcgccttt tcgaaaacct agtagttaat 60
277 attcatttgt ttaaatctta ttttattttt aagctcaaac tgcttaagaa taccttaatt 120
278 ccttaaagtg aaataatttt ttgcaaaggg gtttcctcga tttggagctt tttttttott 180
279 ccaccgtcat ttctaactct taaaaccaac tcagttccat c atg gtg atg ttc aag 236
280 Met Val Met Phe Lys
281 1 5
283 aag atc aag tct ttt gag gtg gtc ttt aac gac cct gaa aag gtg tac 284
284 Lys Ile Lys Ser Phe Glu Val Val Phe Asn Asp Pro Glu Lys Val Tyr
285 10 15 20
287 ggc agt ggc gag agg gtg gct ggc cgg gtg ata gtg gag gtg tgt gaa 332
288 Gly Ser Gly Glu Arg Val Ala Gly Arg Val Ile Val Glu Val Cys Glu
289 25 30 35
291 gtt act cgt gtc aaa gcc gtt agg atc ctg gct tgc gga gtg gct aaa 380
292 Val Thr Arg Val Lys Ala Val Arg Ile Leu Ala Cys Gly Val Ala Lys
293 40 45 50
295 gtg ctt tgg atg cag gga tcc cag cag tgc aaa cag act tcg gag tac 428
296 Val Leu Trp Met Gln Gly Ser Gln Gln Cys Lys Gln Thr Ser Glu Tyr
297 55 60 65
299 ctg cgc tat gaa gac acg ctt ctt ctg gaa gac cag cca aca ggt gag 476

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/934,249

DATE: 10/17/2001

TIME: 12:05:08

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10172001\I934249.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14

L:1106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17

L:1107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17

L:1112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17